

Figure 1

1 M-----ARAKLPRSPSE-----GKAGPGGA-----PAGAAAPEE hSlo2
1 M-----ARAKLPRSPSE-----GKAGPGDT-----PAGSAAPEE rSLACK
1 AREEGGGSHSLPRVGSSELPGRMPLPDGARTGGVCREARGGYTNRTTFEFDQCAPRR KIAA1422

30 P-HGLSPLLPARG--GGSVGSVDV--GORLPVEDFSLDSSLSQ---VOVEFYVNENTFK hSlo2
30 P-HGLSPLLPLETRG--GGSVGSVDV--GORLHVEDFSLDSSLSQ---VOVEFYVNENTFK rSLACK
61 PCAGDGALLDITAGFKMSDLDSEVLPLPFRYRFRDLLEGGDPSFQNDNR VOVEFYVNENTFK KIAA1422

80 ERLKLPFIKNORSSLRIRLFNFSKLLTCLLYIVRVLLDDPALGIGCWGCPKONYSFNDS hSlo2
80 ERLKLPFIKNORSSLRIRLFNFSKLLTCLLYIVRVLLDDPALGIGCWGCPKONYSFNDS rSLACK
121 ERLKLPFIKNORSSLRIRLFNFSKLLTCLLYIVRVLLDDPALGIGCWGCPKONYSFNDS KIAA1422

140 SSEINWAPILWVERKMTLWAIQVIVAIISFLETMLLIYLSYKGNIEWEQIFRVSPVLEMIN hSlo2
140 SSEFHWAPILWVERKMTLWAIQVIVAITISFLETMLLIYLSYKGNIEWEQIFRVSPVLEMIN rSLACK
181 SSEINWAPILWVERKMTLWAIQVIVAIISFLETMLLIYLSYKGNIEWEQIFRVSPVLEMIN KIAA1422

200 TLFFIITIFWPPPLNLFIPVFLNCLWAKHALENMINDFHRAILRTQSAMFNQVLILFCTL hSlo2
200 TLFFIITIFWPPPLNLFIPVFLNCLWAKHALENMINDFHRAILRTQSAMFNQVLILFCTL rSLACK
241 TLFFIITIFWPPPLNLFIPVFLNCLWAKHALENMINDFHRAILRTQSAMFNQVLILFCTL KIAA1422

260 LCLVFTGTCTGCIQHLEKAGENLSLLTSFYFCIVTFSTVGYGDTVTPKIWPSOLLVVMICVA hSlo2
260 LCLVFTGTCTGCIQHLEKAGENLSLLTSFYFCIVTFSTVGYGDTVTPKIWPSOLLVVMICVA rSLACK
301 LCLVFTGTCTGCIQHLEKAGENLSLLTSFYFCIVTFSTVGYGDTVTPKIWPSOLLVVMICVA KIAA1422

320 LVVLPLOFEELVYLWNEROKSGGNYSRHRAOTEKHVVLCVSSLKIDLLMDFLNEFYAHRP hSlo2
320 LVVLPLOFEELVYLWNEROKSGGNYSRHRAOTEKHVVLCVSSLKIDLLMDFLNEFYAHRP rSLACK
361 LVVLPLOFEELVYLWNEROKSGGNYSRHRAOTEKHVVLCVSSLKIDLLMDFLNEFYAHRP KIAA1422

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380 LQDYVVVILCPTSEMDVQVRRVLOIPLWSORVIYLOGSALKDQDLMRKMDNNGEACFILSS rSLACK
421 LQDYVVVILCPTSEMDVQVRRVLOIPLWSORVIYLOGSALKDQDLMRKMDNNGEACFILSS KIAA1422

440 RNEVDRTAADHQTILRAWAVKDFAPNCPLYVOILKPKENKPHVKFADHVVCEBECKYAMLA hSlo2
440 RNEVDRTAADHQTILRAWAVKDFAPNCPLYVOILKPKENKPHVKFADHVVCEBECKYAMLA rSLACK
481 RNEVDRTAADHQTILRAWAVKDFAPNCPLYVOILKPKENKPHVKFADHVVCEBECKYAMLA KIAA1422

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500 LNCICPATSTLITILLVHTSRGOEGOESPEQWORMYGRCSGNEVYHIRMGDSKFFREYEGK rSLACK
541 LNCICPATSTLITILLVHTSRGOEGOESPEQWORMYGRCSGNEVYHIRMGDSKFFREYEGK KIAA1422

560 SFTYAAPFAHKKYGVCLIGLKREDNKSILLNPGPRHILAASDTCFYINITKEENSAPIFK hSlo2
560 SFTYAAPFAHKKYGVCLIGLKREDNKSILLNPGPRHILAASDTCFYINITKEENSAPIFK rSLACK
601 SFTYAAPFAHKKYGVCLIGLKREDNKSILLNPGPRHILAASDTCFYINITKEENSAPIFK KIAA1422

620 QEEKRRKKRAFSGOGLHEGPARLPVHSIIASM--VAMDLOGTEHRPTOSGGGGGSKLALP hSlo2
620 QEBKQNRRLGLAGGALYEGPSRLPVHSIIASM--VAMDLOGNTDCRPSGGGGGSKLTLP rSLACK
661 QEEKRRKKRAFSGOGLHEGPARLPVHSIIASMTGVAMDLOGTEHRPTOSGGGGGSKLALP KIAA1422

678 TENGSGSRRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP hSlo2
678 TENGSGSRRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP rSLACK
721 TENGSGSRRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP KIAA1422

738 YIVSSPTLCHLLLPVKAPFCCLRLDGCKKHNSYEDAKAYGFKNKLIIVSAETAGNGLYNFI hSlo2
738 YIGSSPTLCHLLLPVKAPFCCLRLDGCKKHNSYEDAKAYGFKNKLIIVSAETAGNGLYNFI rSLACK
781 YIGSSPTLCHLLLPVKAPFCCLRLDGCKKHNSYEDAKAYGFKNKLIIVSAETAGNGLYNFI KIAA1422

798 VPLRAYYRSRKELNPIVLLLDNKPDDHFLAICCFPMVYYMEGSVDNLDLSLLOCGIYYAD hSlo2
798 VPLRAYYRSRKELNPIVLLLDNKPDDHFLAICCFPMVYYMEGSVDNLDLSLLOCGIYYAD rSLACK
841 VPLRAYYRSRKELNPIVLLLDNKPDDHFLAICCFPMVYYMEGSVDNLDLSLLOCGIYYAD KIAA1422

858 NLVVVDKESTMSAREEDYMADAktivNVQTMFRLFPPLSLITTELTHPSNMRFMOFRAKDSY hSlo2
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901 NLVVVDKESTMSAREEDYMADAktivNVQTMFRLFPPLSLITTELTHPSNMRFMOFRAKDSY KIAA1422

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1021 DTPPGSGYLCAMKITEGDLWIRTYGRFLFOKLCSSSAEIPIGIYRTESHVFTSEPHDLR KIAA1422

1038 OSOISVNVDECDTREVKGPWGSRACTGGSS--OGRHTGGGDPAEHPLLRRKSLowARRLS hSlo2
1037 OSOISVNVDECDTREVKGPWGSRACTGGSS--OGRHTGGGDPAEHPLLRRKSLowARRLS rSLACK
1081 OSOISVNVDECDTREVKGPWGSRACTGGSS--OGRHTGGGDPAEHPLLRRKSLowARRLS KIAA1422

1097 RKAPKOAGRAA--AAEHSOORLSLYRRSEROELSELVKNRMKHLGLPTTGIEDVANLTAS hSlo2
1097 RKSSKOAGKAPMTTDWITQORLSLYRRSEROELSELVKNRMKHLGLPTTGIEDVANLTAS rSLACK
1140 RKAPKOAGRAA--A KIAA1422

1156 DVMNRVNLGYLODEMNDH--ONTLSYVLINPPPDTRLEPSDIVYLIRSDPLAHVASSSSOSR hSlo2
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KIAA1422

1215 KSSCSHKLSSCNPETRDETOL hSlo2
1217 KSSCSNKLSSCNPETRDETOL rSLACK
KIAA1422

09927369 "00000000"

Figure 2

1 MV-----DLESEVPFLPPRYRFRD LLL---GDQGWQND DR----- Slo4
 1 MARAKLPRSPSE GKAGPGGAPAGAAAPDEEPH-GLSP LLPARGGGSVGS DVGQRLPVEDFS Slo2

33 -----VQVEFYMNENTFKERLKLFFIKNQSSLRIRLFNFSLKLLSCLLYIIRVLLLEN Slo4
 60 LDSSLSQVQVEFYVNENTFKERLKLFFIKNQSSLRIRLFNFSLKLLTCLLYIIVRVLLDD Slo2

86 PSQGN-----EWSHIFWVNRSLPLWGLQVSVVALISL FETILLGYLS Slo4
 120 PALGIGCWGCPKQNYSFNDSSSEINWAPILWVERKMTLWAIQVI VAIISFLETMLLIYLS Slo2

127 YKGNIEWEQILRIPFILEIINAVPFIISIFWPSLRNLFPVFLNCWLAKHALENMINDLHR Slo4
 180 YKGNIEWEQIFRVSFVLEMINTLFFIITIFWPLRLNLFPVFLNCWLAKHALENMINDFHR Slo2

187 AIQRTQSAMFNQVLILISTLLCLIFTCICGIOHLERIGKKLNLFD SLYFCIVTFSTVGF Slo4
 240 AILRTQSAMFNQVLILFCTLLCLVFTGTGCGIOHLERA GENLSLLTSFYFCIVTFSTVGYG Slo2

247 DVTPETWSKLFVVA MICVALVVLPIQFEQLAYLWMERQKSGGNYSRHRAQTEKHVVL CV Slo4
 300 DVTPKIWPSQLLVIMICVALVVLPLQFEBLVYLWMERQKSGGNYSRHRAQTEKHVVL CV Slo2

307 SSLKIDLLMDFLNEFYAHPRLQDYVVILCPTEMDVQVRRVLQIPLMWSQRVIY LQGSALK Slo4
 360 SSLKIDLLMDFLNEFYAHPRLQDYVVILCPTEMDVQVRRVLQIPLMWSQRVIY LQGSALK Slo2

367 DQDLLRAKMDDAEACFILSSRC EVDRTSSDHQTLRAWAVKDFAPNCP LYVQILKPENKF Slo4
 420 DQDLMRAKMDNGEACFILSSRN EVDRTAA DHQTLRAWAVKDFAPNCP LYVQILKPENKF Slo2

427 HIKFADHVVC EEFKYAMLALNCICPATSTLITLLVHTSRGQEGQ QSPEQWQKMYGRCSG Slo4
 480 HVKFADHVVC EEFKYAMLALNCICPATSTLITLLVHTSRGQEGQE SPEQWQRMYGRCSG Slo2

487 NEVYHIVLEES TFFAEYEGKSFTYAS FFAHKKFGVCLIGVR REDNKN ILLNPGPRYIMNS Slo4
 540 NEVYHIRMGDS KFFREYEGKSFTYAA FFAHKKYGVCLIGLKR EDNKS ILLNPGPRHILAA Slo2

547 TDI CFYINITKEENSAF--KNQDQQRKSNVS-RSPFYHGPSRLPVHSIIASMGTVAIDLQD Slo4
 600 SDTCFYINITKEENSAFIFKQEEKRK KRAFSGQGLHEGPARLPVHSIIASM--VAMD LQG Slo2

604 TSCRSA-----SGPTLSLPTEGSKEIRRRPSIAPVLEVADTSSSIQT CDLLSDQSEDETTP Slo4
 658 TEHRPTQSGGGGGGSKLALPTENGSGSRRPSIAPVLELADSSALLP CDLLSDQSEDEVTP Slo2

658 -DEEMSSNL EYAKGYPPYSPYIIGSSPTFCHLLHKKVPFCCLRLDKSCQHNY YEDAKAYGF Slo4
 718 SDDEGLSVV EYVKGYPN SPYIIVSSPTLCHLLPVKAPFCCLRLDKGCKHNS YEDAKAYGF Slo2

717 KNKLIIVA AETAGNGLYNFIVPLRAYYRPKKELNPIVLLLDNPPDMHFLDAICWFPMVYY Slo4
 778 KNKLIIVS AETAGNGLYNFIVPLRAYYRSRKELNPIVLLLDNKPDMHFLDAICCFPMVYY Slo2

777 MVGSI DNLD DLR CGVTFAANM VVVDKESTMSAEEDYMADAKTIVNVQTLFRLFPSSLSII Slo4
 838 MEGSV DNLD SLLQCGIIYADNL VVVDKESTMSAEEDYMADAKTIVNVQTMFRLFPSSLSIT Slo2

837 TELTHPANNMRFMQFRAKDCYSLALSKLEKKEREREGSNLAFNFRLPFAAGRVFSISM LDTL Slo4
 898 TELTHPANNMRFMQFRAKDSYSLALSKLEKKREREMGSNLAFNFRLPFAAGRVFSISM LDTL Slo2

897 LYQSFVKDYMI SITRLLLGLD TTGSGF LSCMKITADDLWIRTYARLYQKLCSSSTGDVPI Slo4
 958 LYQSFVKDYMITITRLLLGLD TTGSGYLCA MKITEGDLWIRTYGR LFQKLCSSSAEIPISlo2

957 GIYRTESQKLT TSE-----SQISISVEEWEDTKDSKEQGHHR-----SNHRNSTSSD Slo4
 1018 GIYRTESHVFTSEPHDLRAQSQISVNVEDCEDTREVKGPWGSRA GTGSSQGRHTGGGD Slo2

1004 QSDHPLLRRKSMQWARRLSRKGP KHS GKTA--EKITQORLNLYRRSERQELAE LVKNRMK Slo4
 1078 PAEHPLLRRKSLQWARRLSRKAPKQAGRAAAAEWISQORLSLYRRSERQELS ELVKNRMK Slo2

1062 HLG LSTVGY-----DEMNDHQSTLSYI LINPSPDTRIELNDV VY Slo4
 1138 HLG LPTTGYEDVANLTASDV MNRVNLGYLQDEMNDHQNTLSYV LIMPSPDTRLEPSDIVY Slo2

1101 LIRPDPLAYLPN SEP SRNSI CNVT---GQDSREBTQL Slo4
 1198 LIRSDPLAHVAS SSQSRKSS-C SHKLSSCNPETRDETOL Slo2

05931159 "000101

Figure 3

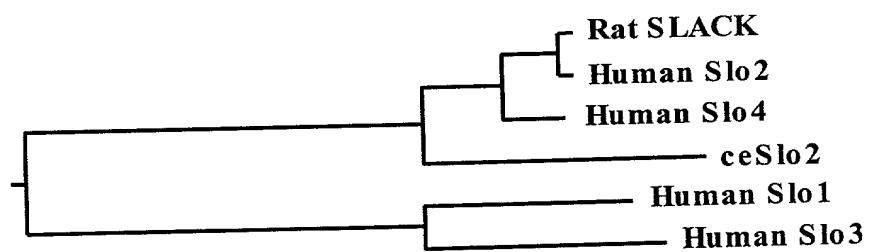
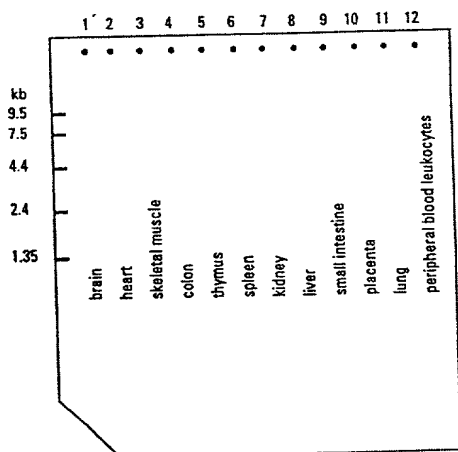


Figure 4



	1	2	3	4	5	6	7	8
A	whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
B	occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
C	heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
D	testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
E	kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta				
G	fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	
H	yeast total RNA 100 ng	yeast rRNA 100 ng	<i>E. coli</i> rRNA 100 ng	<i>E. coli</i> DNA 100 ng	Poly r(A) 100 ng	human C ₁ DNA 100 ng	human DNA 100 ng	human DNA 500 ng

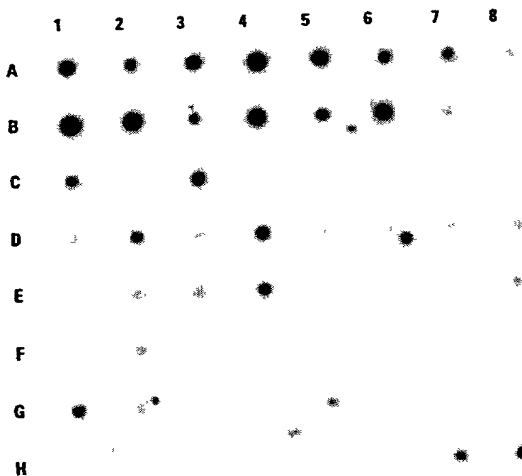
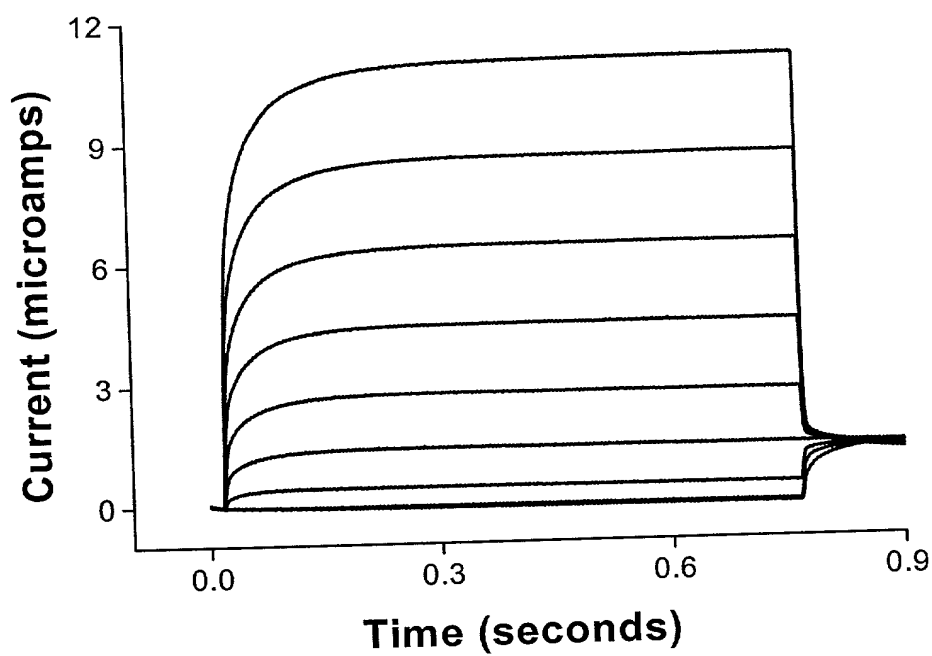


Figure 5

A



B

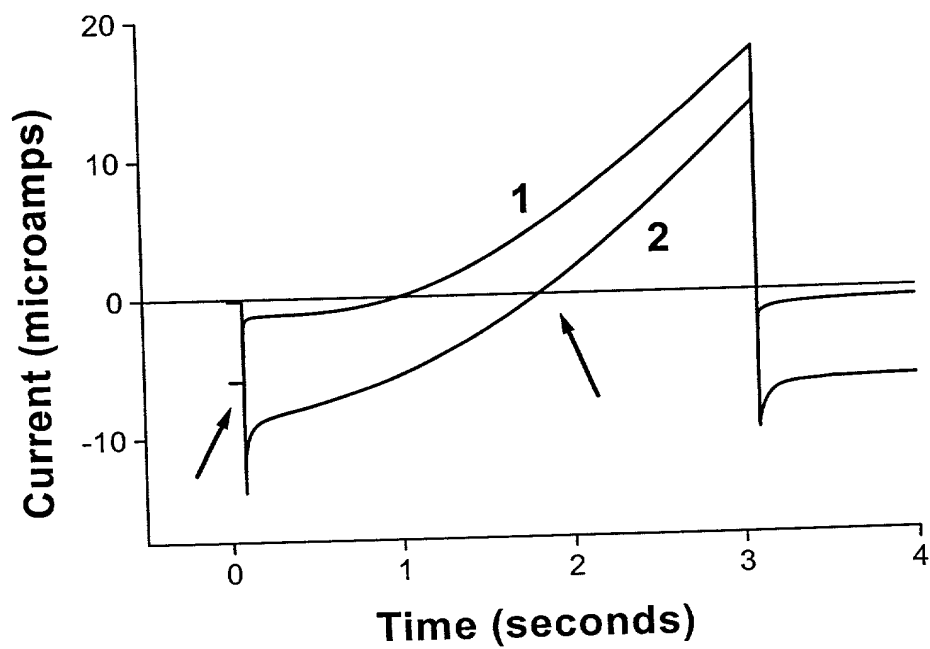
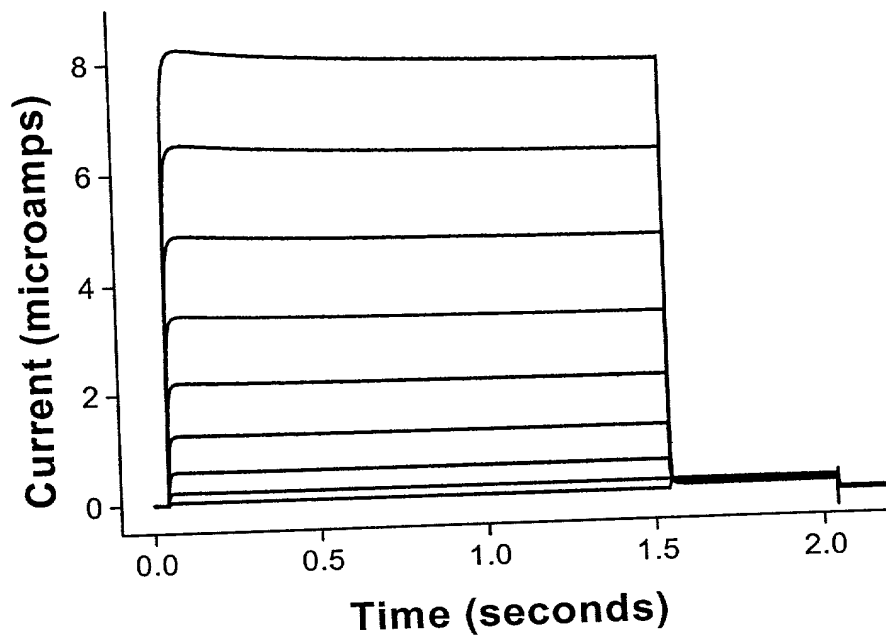


Figure 6

A



B

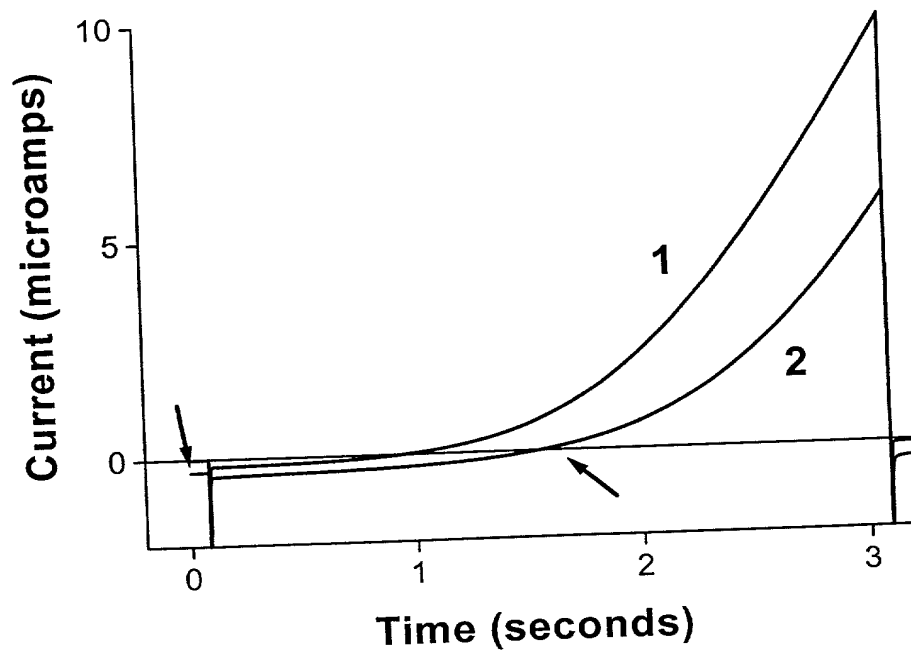


Figure 7A

Slo4 Northern Blot

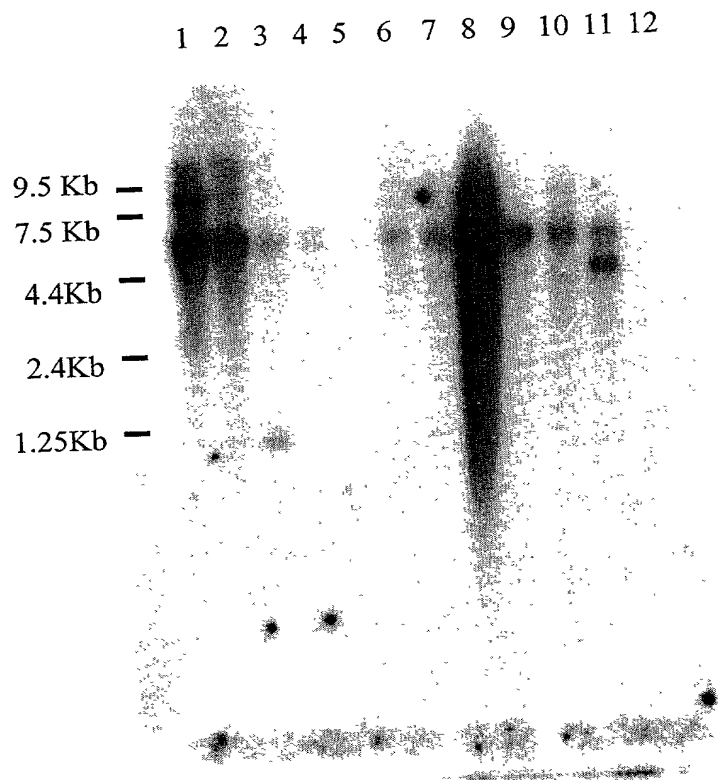


Figure 7 B

Slo4 mRNA Dot Blot

	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum, left	substantia nigra	heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum, right	nucleus accumbens	aorta	stomach	colon, descending	skeletal muscle	placenta	pancreas	Hela S3	fetal heart	yeast tRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia, K-562	fetal kidney	<i>E. coli</i> rRNA
D	parietal lobe	amygdala	pituitary gland	atrium, right	jejunum		thymus	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	<i>E. coli</i> DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricle, left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	poly (A)
F	temporal lobe	hippocampus		ventricle, right	ileocecum		lymph node	testis	mammary gland	Burkitt's lymphoma, Daudi	fetal thymus	human t-Cyt. 1 DNA
G	p.g.* of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adenocarcinoma, SW460	fetal lung	human DNA 100 ng
H	pons	putamen		apex of the heart	colon, ascending		trachea			lung carcinoma, A549		human DNA 500 ng

* para-central gyrus

